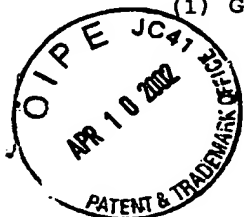


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SEQUENCE LISTING

APR 12 2002

TECH CENTER 1600/2900



(1) GENERAL INFORMATION:

- (i) APPLICANT: Jaye, Michael C.  
Lynch, Kevin J.  
Amin, Dilip V.  
Doan, Kim-Anh T.  
Marchadier, Dawn  
Maugeais, Cyrille  
Rader, Daniel J.  
Krawiec, John A.  
South, Victoria J.
- (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EFFECTING THE LEVELS OF HIGH DENSITY LIPOPROTEIN (HDL) CHOLESTEROL AND APOLIPOPROTEIN AI, VERY LOW DENSITY LIPOPROTEIN (VLDL) CHOLESTEROL AND LOW DENSITY LIPOPROTEIN (LDL) CHOLESTEROL
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Synnestvedt & Lechner LLP  
(B) STREET: Suite 2600 Aramark Tower, 1101 Market Street  
(C) CITY: Philadelphia  
(D) STATE: PA  
(E) COUNTRY: USA  
(F) ZIP: 19107
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-Windows 95  
(D) SOFTWARE: Corel WordPerfect 8.0 converted to ASCII
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/277,401  
(B) FILING DATE: March 26, 1999  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Kelly, Ph.D., Patrick J.  
(B) REGISTRATION NUMBER: 34,638  
(C) REFERENCE/DOCKET NUMBER: 22,944-C USA
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (215) 923-4466  
(B) TELEFAX: (215) 923-2189

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 22..180
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| GAATTCGGCT | TGATCAATCG | C   | TTC | AAA | AAG | GGG | ATC | TGT | CTG | AGC | TGC | CGC | 51  |     |     |    |
|            |            |     | Phe | Lys | Lys | Gly | Ile | Cys | Leu | Ser | Cys | Arg |     |     |     |    |
|            |            |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |    |
| AAG        | AAC        | CGT | TGT | AAT | AGC | ATT | GGC | TAC | AAT | GCC | AAG | AAA | ATG | AGG | AAC | 99 |
| Lys        | Asn        | Arg | Cys | Asn | Ser | Ile | Gly | Tyr | Asn | Ala | Lys | Lys | Met | Arg | Asn |    |
|            |            |     | 15  |     |     |     | 20  |     |     |     |     |     | 25  |     |     |    |

AAG AGG AAC AGC AAA ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC	147
Lys Arg Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe	
30 35 40	
AGA GGT AAC CTT CAG TCC CTG GAG TGT CCC TGA GGAAGGCCCT TAATACCTCC	200
Arg Gly Asn Leu Gln Ser Leu Glu Cys Pro	
45 50	
TTCTTAATAC CATGCTGCAG AGCAGGGCAC ATCCTAGCCC AGGAGAAGTG GCCAGCACAA	260
TCCAATCAAA TCGTTGCAAA TCAGATTACA CTGTGCATGT CCTAGGAAAG GGAATCTTTA	320
CAAAATAAAC AGTGTGGACC CCTCAAAAAA AAAAAAAGC CGAATTC	367

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg	Cys	Asn	Ser
1				5					10					15	
Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg	Asn	Ser	Lys	Met
			20					25					30		
Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg	Gly	Asn	Leu	Gln	Ser
		35					40						45		
Leu	Glu	Cys	Pro												
		50													

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 312..1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCT TCTACTACTA CTAGGCCACG CGTCGCCTAG TACGGGGGGG GGGGGGGGGG	60
TCAGCGAGTC CTGCGCTCCC GGCGGCTCAG GACGAGGGCA GATCTCGTTC TGGGGCAAGC	120
CGTTGACACT CGCTCCCTGC CACCGCCCGG GCTCCGTGCC GCCAAGTTT CATTTTCCAC	180
CTTCTCTGCC TCCAGTCCCC CAGCCCCTGG CCGAGAGAAG GGTCTTACCG GCCGGGATTG	240
CTGGAAACAC CAAGAGGTGG TTTTGTGTTT TTAAACTTC TGTTCTTGG GAGGGGGTGT	300
GGCGGGGCAG G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC	350
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu	
1 5 10	
TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA	398
Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly	
15 20 25	
CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC	446
Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val	
30 35 40 45	
AAA CCA TCT GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT	494
Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His	
50 55 60	
GAA GGA TGC TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC	542
Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys	
65 70 75	
AGT TTC AAC ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG	590
Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr	
80 85 90	

71  
cont.

ATG AGC GGT ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG 638  
 Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu  
 95 100 105  
 CAC ACA AGA GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC 686  
 His Thr Arg Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro  
 110 115 120 125  
 CTG GCC CAC CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG 734  
 Leu Ala His Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val  
 130 135 140  
 GGA CAC AGC ATT GCC AGG ATG CTC GAC TGG CTG CAG GAG AAG GAC GAT 782  
 Gly His Ser Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp  
 145 150 155  
 TTT TCT CTC GGG AAT GTC CAC TTG ATC GGC TAC AGC CTC GGA GCG CAC 830  
 Phe Ser Leu Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His  
 160 165 170  
 GTG GCC GGG TAT GCA GGC AAC TTC GTG AAA GGA ACG GTG GGC CGA ATC 878  
 Val Ala Gly Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile  
 175 180 185  
 ACA GGT TTG GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC 926  
 Thr Gly Leu Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His  
 190 195 200 205  
 AAG AGG CTC TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC 974  
 Lys Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr  
 210 215 220  
 TAC ACG CGT TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC 1022  
 Tyr Thr Arg Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly  
 225 230 235  
 CAC ATT GAC ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA 1070  
 His Ile Asp Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly  
 240 245 250  
 CTC AAC GAT GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG 1118  
 Leu Asn Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val  
 255 260 265  
 GTA AAA TGT GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG 1166  
 Val Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu  
 270 275 280 285  
 GTG AAT CAG GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT 1214  
 Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn  
 290 295 300  
 CGC TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT 1262  
 Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn  
 305 310 315  
 AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA 1310  
 Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys  
 320 325 330  
 ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC AGA GGT AAC CTT CAG 1358  
 Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln  
 335 340 345  
 TCC CTG GAG TGT CAAGCCGAAT TC 1382  
 Ser Leu Glu Cys  
 350

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys  
 1 5 10 15

Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu  
 20 25 30  
 Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser  
 35 40 45  
 Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys  
 50 55 60  
 Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn  
 65 70 75 80  
 Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly  
 85 90 95  
 Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg  
 100 105 110  
 Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His  
 115 120 125  
 Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser  
 130 135 140  
 Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu  
 145 150 155 160  
 Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly  
 165 170 175  
 Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu  
 180 185 190  
 Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu  
 195 200 205  
 Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg  
 210 215 220  
 Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp  
 225 230 235 240  
 Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp  
 245 250 255  
 Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys  
 260 265 270  
 Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln  
 275 280 285  
 Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys  
 290 295 300  
 Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly  
 305 310 315 320  
 Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu  
 325 330 335  
 Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu  
 340 345 350  
 Cys

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC TGC TAT TGC  
 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys  
 1 5 10 15

48

TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA CGG CTG GAA

96